



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gorman, Daniel M.
Randall, Troy D.
Zlotnik, Albert

(ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED REAGENTS

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/911,423
(B) FILING DATE: 14-AUG-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/023,419
(B) FILING DATE: 16-AUG-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/027,901
(B) FILING DATE: 07-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: DX0612K

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1073 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

70640X

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64

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(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 68..751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGAGATCC ATTGTGCTGG AAAGGGAACCT CCTGAAATCA GCCGACAGAA GACTCAGGAG 60

AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT 109
Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys
1 5 10

GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC 157
Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Pro Gly Cys Gly
15 20 25 30

CCT GGC AAG GTT CAG AAC GGA AGT GGC AAC AAC ACT CGC TGC TGC AGC 205
Pro Gly Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser
35 40 45

CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT 253
Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys
50 55 60

GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG 301
Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys
65 70 75

CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT 349
His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile
80 85 90

GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA 397
Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala
95 100 105 110

GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA 445
Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly
115 120 125

TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC 493
Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile
130 135 140

CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC 541
Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe
145 150 155

CTG GTC ATG GCT GCA TGC ATT TTC TTC CTA ACC ACA GTC CAG CTC GGC 589
Leu Val Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly
160 165 170

CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC 637

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Leu	His	Ile	Trp	Gln	Leu	Arg	Arg	Gln	His	Met	Cys	Pro	Arg	Glu	Thr	
175					180					185					190	
CAG	CCA	TTC	GCG	GAG	GTG	CAG	TTG	TCA	GCT	GAG	GAT	GCT	TGC	AGC	TTC	685
Gln	Pro	Phe	Ala	Glu	Val	Gln	Leu	Ser	Ala	Glu	Asp	Ala	Cys	Ser	Phe	
				195					200					205		
CAG	TTC	CCT	GAG	GAG	GAA	CGC	GGG	GAG	CAG	ACA	GAA	GAA	AAG	TGT	CAT	733
Gln	Phe	Pro	Glu	Glu	Glu	Arg	Gly	Glu	Gln	Thr	Glu	Glu	Lys	Cys	His	
			210					215					220			
CTG	GGG	GGT	CGG	TGG	CCA	TGAGGCCTGG	TCTTCCTCTG	TGCCCCAAGC								781
Leu	Gly	Gly	Arg	Trp	Pro											
			225													
CAGACGCTAC	AAGACTTGCC	CAGCTATAACC	CTTGGTGAGA	GCAGGGGCCA	TGCTCTGCAC											841
CCTTCCCTGG	GCCTGGCCCT	GCTCCCCTCA	ACAGTGGCGG	AAGTGGGTGT	ATGAGAGCGG											901
TGAGTTACGA	TTGGGGCCCTA	TGGCTGCCTT	TCTCATTTGA	CAGCTCTGTT	GGAGTAGGGT											961
CTTTGGGCCC	ACCAAGAGCA	CCACGTTTAG	CACAAGATCT	TGTACAAGAA	TAAATACTTG											1021
TTTAGTAACC	TGAAAAAAAAA	AAAAAAAAAGG	GCGGCCGCGG	AGGCCGAATT	CC											1073

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 228 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Ala	Trp	Ala	Met	Leu	Tyr	Gly	Val	Ser	Met	Leu	Cys	Val	Leu	
1				5				10					15			
Asp	Leu	Gly	Gln	Pro	Ser	Val	Val	Glu	Glu	Pro	Gly	Cys	Gly	Pro	Gly	
			20					25					30			
Lys	Val	Gln	Asn	Gly	Ser	Gly	Asn	Asn	Thr	Arg	Cys	Cys	Ser	Leu	Tyr	
		35					40					45				
Ala	Pro	Gly	Lys	Glu	Asp	Cys	Pro	Lys	Glu	Arg	Cys	Ile	Cys	Val	Thr	
	50					55					60					
Pro	Glu	Tyr	His	Cys	Gly	Asp	Pro	Gln	Cys	Lys	Ile	Cys	Lys	His	Tyr	
65					70				75					80		
Pro	Cys	Gln	Pro	Gly	Gln	Arg	Val	Glu	Ser	Gln	Gly	Asp	Ile	Val	Phe	
				85				90						95		
Gly	Phe	Arg	Cys	Val	Ala	Cys	Ala	Met	Gly	Thr	Phe	Ser	Ala	Gly	Arg	
			100					105						110		

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Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly Phe Leu
 115 120 125
 Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile Pro Glu
 130 135 140
 Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe Leu Val
 145 150 155 160
 Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly Leu His
 165 170 175
 Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr Gln Pro
 180 185 190
 Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe Gln Phe
 195 200 205
 Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His Leu Gly
 210 215 220
 Gly Arg Trp Pro
 225

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GCA CAG CAC GGG GCG ATG GGC GCG TTT CGG GCC CTG TGC GGC CTG	48
Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu	
1 5 10 15	
GCG CTG CTG TGC GCG CTC AGC CTG GGT CAG CGC CCC ACC GGG GGT CCC	96
Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro	
20 25 30	
GGG TGC GGC CCT GGG CGC CTC CTG CTT GGG ACG GGA ACG GAC GCG CGC	144
Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg	
35 40 45	
TGC TGC CGG GTT CAC ACG ACG CGC TGC TGC CGC GAT TAC CCG GGC GAG	192
Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu	
50 55 60	

GAG TGC TGT TCC GAG TGG GAC TGC ATG TGT GTC CAG CCT GAA TTC CAC	240
Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His	
65 70 75 80	
TGC GGA GAC CCT TGC TGC ACG ACC TGC CGG CAC CAC CCT TGT CCC CCA	288
Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro	
85 90 95	
GGC CAG GGG GTA CAG TCC CAG GGG AAA TTC AGT TTT GGC TTC CAG TGT	336
Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys	
100 105 110	
ATC GAC TGT GCC TCG GGG ACC TTC TCC GGG GGC CAC GAA GGC CAC TGC	384
Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys	
115 120 125	
AAA CCT TGG ACA GAC TGC ACC CAG TTC GGG TTT CTC ACT GTG TTC CCT	432
Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro	
130 135 140	
GGG AAC AAG ACC CAC AAC GCT GTG TGC GTC CCA GGG TCC CCG CCG GCA	480
Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala	
145 150 155 160	
GAG CCG CTT GGG TGG CTG ACC GTC GTC CTC CTG GCC GTG GCC GCC TGC	528
Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys	
165 170 175	
GTC CTC CTC CTG ACC TCG GCC CAG CTT GGA CTG CAC ATC TGG CAG CTG	576
Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu	
180 185 190	
AGG AGT CAG TGC ATG TGG CCC CGA GAG ACC CAG CTG CTG CTG GAG GTG	624
Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val	
195 200 205	
CCG CCG TCG ACC GAA GAC GCC AGA AGC TGC CAG TTC CCC GAG GAA GAG	672
Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu	
210 215 220	
CGG GGC GAG CGA TCG GCA GAG GAG AAG GGG CGG CTG GGA GAC CTG TGG	720
Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp	
225 230 235 240	
GTG TGAGCCTGGC CGTCCTCCGG GGCCACCGAC CGCAGCCAGC CCCTCCCCAG	773
Val	
GAGCTCCCCA GGCCGCAGGG GCTCTGCGTT CTGCTCTGGG CCGGGCCCTG CTCCCCTGGC	833
AGCAGAAGTG GGTGCAGGAA GGTGGCAGTG ACCAGCGCCC TGGACCATGC AGTTCGGCGG	893
CCGCTCTAAA GGATCCAAGC TTACGTACGC GTGCATGCGA CGTCATAGCT CTTCTATAGT	953
GTCACCTAAA TTCAATTAC TGGCCGTCGT TTTACAACGT CCTGACTGGG AAA	1006

(2) INFORMATION FOR SEQ ID NO:4:

68

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
1 5 10 15
Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
20 25 30
Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
35 40 45
Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
50 55 60
Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
65 70 75 80
Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
85 90 95
Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
100 105 110
Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
115 120 125
Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
130 135 140
Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
145 150 155 160
Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
165 170 175
Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
180 185 190
Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
195 200 205
Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
210 215 220
Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
225 230 235 240
Val

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCNCARC AYGGNGCNAT GGGNGCNTTY MGNGCNYTNT GYGGNYTNGC NYTNYTNTGY 60
GCNYTNWSNY TNGGNCARMG NCCNACNGGN GGNCNGGNT GYGGNCCNGG NMGNYTNYTN 120
YTNGGNACNG GNACNGAYGC NMGNTGYTGY MGNGTNCAYA CNACNMGNTG YTG YMGNGAY 180
TAYCCNGGNG ARGARTGYTG YWSNGARTGG GAYTGYATGT GYGTNCARCC NGARTTYCAY 240
TGYGGNGAYC CNTGYTGYAC NACNTGYMGN CAYCAYCCNT GYCCNCCNGG NCARGGNGTN 300
CARWSNCARG GNAARTTYWS NTTYGGNTTY CARTGYATHG AYTGYGCNWS NGGNACNTTY 360
WSNGGNGGNC AYGARGGNCA YTG YAARCCN TGGACNGAYT GYACNCARTT YGGNTTYTNYTN 420
ACNGTNTTYC CNGGNAAYAA RACNCAYAA Y GCNGTNTGYG TNCCNGGNWS NCCNCCNGCN 480
GARCCNYTNG GNTGGYTNAC NGTNGTNYTN YTNGCNGTNG CNGCNTGYGT NYTNYTNYTN 540
ACNWSNGCNC ARYTNGGNYT NCAYATHTGG CARYTNMGNW SNCARTGYAT GTGGCCNMGN 600
GARACNCARY TNYTNYTNGA RGTNCCNCCN WSACNGARG AYGCNMGNWS NTGYCARTTY 660
CCNGARGARG ARMGNGGNGA RMGNWSNGCN GARGARAARG GNMGNYTNGG NGAYYTNTGG 720
GTN 723

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu
1 5 10 15

Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
 20 25 30
 Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
 35 40 45
 Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp
 50 55 60
 Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys
 65 70 75 80
 Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser
 85 90 95
 Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys Ile Asp Cys Ala Ser Gly
 100 105 110
 Thr Phe Ser Gly Gly His Glu Gly His Cys Lys Pro Trp Thr Asp Cys
 115 120 125
 Thr Gln Phe Gly Phe Leu Thr Val Phe Pro Gly Asn Lys Thr His Asn
 130 135 140
 Ala Val Cys Val Pro Gly Ser Pro Pro Ala Glu Pro Leu Gly Trp Leu
 145 150 155 160
 Thr Val Val Leu Leu Ala Val Ala Ala Cys Val Leu Leu Leu Thr Ser
 165 170 175
 Ala Gln Leu Gly Leu His Ile Trp Gln Leu Arg Lys Thr Gln Leu Leu
 180 185 190
 Leu Glu Val Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro
 195 200 205
 Glu Glu Glu Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly
 210 215 220
 Asp Leu Trp Val
 225

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

71

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Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu
 1 5 10 15
 Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
 20 25 30
 Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
 35 40 45
 Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp
 50 55 60
 Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys
 65 70 75 80
 Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser
 85 90 95
 Gln Gly Lys Ser Trp Arg Cys Leu Trp Glu Ser Thr Gln Ala Arg Gly
 100 105 110
 Ser Thr Arg Ala Arg Gly Arg Ala Arg Gly His Arg Cys Pro Ala Arg
 115 120 125
 Thr Cys Gly Val Trp Gly Pro Glu Ser Cys Glu Ala Gly Gln Ala Arg
 130 135 140
 Pro Cys Ser Gly Thr Thr Gly His Glu Ala Leu Gly Val Ser Cys Pro
 145 150 155 160
 Cys Phe Leu Ser Leu Gly Phe Ser Ile Gln His Glu Gly Cys Glu Asn
 165 170 175
 Pro Ala Gly Arg Trp Gly Arg Val Pro Gly Ala Val Trp Leu Ser Gly
 180 185 190
 Pro Gly His Pro Ser Cys Leu Ser Ser Pro His Thr Glu Arg Ala Cys
 195 200 205
 Pro Val Pro Pro Gly Val Leu Ser Gly Ala Trp Gly Cys Thr Leu Phe
 210 215 220
 Trp Lys Glu Gln Leu Lys Ser Ser
 225 230

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu
1 5 10 15

Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
20 25 30

Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
35 40 45

Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp
50 55 60

Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys
65 70 75 80

Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser
85 90 95

Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys Ile Asp Cys Ala Ser Gly
100 105 110

Thr Phe Ser Gly Gly His Glu Gly His Cys Lys Pro Trp Thr Asp Cys
115 120 125

Thr Gln Phe Gly Phe Leu Thr Val Phe Pro Gly Asn Lys Thr His Asn
130 135 140

Ala Val Cys Val Pro Gly Ser Pro Pro Ala Glu Pro Leu Gly Trp Leu
145 150 155 160

Thr Val Val Leu Leu Ala Val Ala Ala Cys Val Leu Leu Leu Thr Ser
165 170 175

Ala Gln Leu Gly Leu His Ile Trp Gln Leu Arg Ser Gln Cys Met Trp
180 185 190

Pro Arg Gly Leu Ser Gln Pro Gly Ala Gly Arg Trp Glu His Gly Cys
195 200 205

Leu Leu Thr Val Ala Pro Leu Gln Arg Pro Ser Cys Cys Trp Arg Cys
210 215 220

Arg Arg Arg Pro Lys Thr Pro Glu Ala Ala Ser Ser Pro Arg Lys Ser
225 230 235 240

Gly Ala Ser Asp Arg Gln Arg Arg Arg Gly Gly Trp Glu Thr Cys Gly
245 250 255

Cys Glu Pro Gly Arg Pro Pro Gly Pro Pro Thr Ala Ala Ser Pro Ser
260 265 270

Pro Gly Ala Pro Gln Ala Ala Gly Ala Leu Arg Ser Ala Leu Gly Arg
275 280 285

Ala Leu Leu Pro Trp Gln Gln Lys Trp Val Gln Glu Gly Gly Ser Asp
290 295 300

Gln Arg Pro Gly Pro Cys Ser
305 310

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